

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY11, EXPRESSED HIGHLY IN HEART AND VARIANTS THEREOF

<130> D0075.NP

<150> 60/249,613

<151> 2000-11-17

<150> 60/257,611

<151> 2000-12-21

<150> 60/305,818

<151> 2001-07-16

<160> 81

<170> PatentIn version 3.0

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<212> DNA

<213> homo sapiens

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<222> (515)..(1504)

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tttcactttt ctttgaaatg agcaacctga attactcgga ggagaaaggc aggagagata 180

gaggcagcag aagccagggc agctgaaaga cagagacctt cagtctgaac caacaacaag 240

caaagttaaa ttatggatat ccaagggagt ctatagaagg tccatgcaag acattttgac 300

tacttgctctg aactagatat cccttgaatg tgcacacaaa aagtgaatgg gtcatttgat 360

aagggaaaac taggttccaa gatggctgaa taggaagagc tccagtctgc agatcccagt 420

gtgagcaacg tggaagatgg gtgatttctg catttccaac tgagcatgga gagaaaaatt 480

tatgtccttg caaccatcca tctccgtatc agaa atg gaa cca aat ggc acc ttc 535

Met Glu Pro Asn Gly Thr Phe
1 5

agc aat aac aac agc agg aac tgc aca att gaa aac ttc aag aga gaa 583

Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys Arg Glu

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Asn	Gly	Leu	Ser	Ile	Tyr	Val	Phe	Leu	Gln	Pro	Tyr	Lys	Lys	Ser	Thr		
40					45				50					55			
tct	gtg	aac	gtt	ttc	atg	cta	aat	ctg	gcc	att	tca	gat	ctc	ctg	ttc	727	
Ser	Val	Asn	Val	Phe	Met	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe		
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ata	agc	acg	ctt	ccc	ttc	agg	gct	gac	tat	tat	ctt	aga	ggc	tcc	aat	775	
Ile	Ser	Thr	Leu	Pro	Phe	Arg	Ala	Asp	Tyr	Tyr	Leu	Arg	Gly	Ser	Asn		
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Trp	Ile	Phe	Gly	Asp	Leu	Ala	Cys	Arg	Ile	Met	Ser	Tyr	Ser	Leu	Tyr		
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gtc	aac	atg	tac	agc	agt	att	tat	ttc	ctg	acc	gtg	ctg	agt	gtt	gtg	871	
Val	Asn	Met	Tyr	Ser	Ser	Ile	Tyr	Phe	Leu	Thr	Val	Leu	Ser	Val	Val		
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pgt	ttc	ctg	gca	atg	gtt	cac	ccc	ttt	cgg	ctt	ctg	cat	gtc	acc	agc	919	
Arg	Phe	Leu	Ala	Met	Val	His	Pro	Phe	Arg	Leu	Leu	His	Val	Thr	Ser		
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Ile	Arg	Ser	Ala	Trp	Ile	Leu	Cys	Gly	Ile	Ile	Trp	Ile	Leu	Ile	Met		
				140				145						150			
gct	tcc	tca	ata	atg	ctc	ctg	gac	agt	ggc	tct	gag	cag	aac	ggc	agt	1015	
Ala	Ser	Ser	Ile	Met	Leu	Leu	Asp	Ser	Gly	Ser	Glu	Gln	Asn	Gly	Ser		
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gtc	aca	tca	tgc	tta	gag	ctg	aat	ctc	tat	aaa	att	gct	aag	ctg	cag	1063	
Val	Thr	Ser	Cys	Leu	Glu	Leu	Asn	Leu	Tyr	Lys	Ile	Ala	Lys	Leu	Gln		
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acc	atg	aac	tat	att	gcc	ttg	gtg	gtg	ggc	tgc	ctg	ctg	cca	ttt	ttc	1111	
Thr	Met	Asn	Tyr	Ile	Ala	Leu	Val	Val	Gly	Cys	Leu	Leu	Pro	Phe	Phe		
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Thr	Leu	Ser	Ile	Cys	Tyr	Leu	Leu	Ile	Ile	Arg	Val	Leu	Leu	Lys	Val		
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Glu	Val	Pro	Glu	Ser	Gly	Leu	Arg	Val	Ser	His	Arg	Lys	Ala	Leu	Thr		
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acc	atc	atc	atc	acc	ttg	atc	atc	ttc	ttc	ttg	tgt	ttc	ctg	ccc	tat	1255	
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cac	aca	ctg	agg	acc	gtc	cac	ttg	acg	aca	tgg	aaa	gtg	ggg	tta	tgc	1303	
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Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu Ala Ala			
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gcc aat gcc tgc ttc aat cct ctg ctc tat tac ttt gct ggg gag aat			1399
Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly Glu Asn			
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Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro Gln Lys			
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gca aag aca aag tgt gtt ttc cct gtt agt gtg tgg ttg aga aag gaa			1495
Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg Lys Glu			
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aca aga gta taaggagctc ttagatgaga cctgttcttg tatccttgtg			1544
Thr Arg Val			
330			
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Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu			
35	40	45	
Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu			
50	55	60	
Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp			
65	70	75	80
Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg			

85

90

95

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
100 105 110

Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
115 120 125

Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
130 135 140

Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
145 150 155 160

Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
165 170 175

Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
180 185 190

Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
195 200 205

Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
210 215 220

Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
225 230 235 240

Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
245 250 255

Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
260 265 270

Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
275 280 285

Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
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Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
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Ser Val Trp Leu Arg Lys Glu Thr Arg Val
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 35 40 45

Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
 50 55 60

Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
 65 70 75 80

Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
 85 90 95

Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
 100 105 110

Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
 115 120 125

Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
 130 135 140

Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
 145 150 155 160

Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
 165 170 175

Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
 180 185 190

Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
 195 200 205

Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
 210 215 220

Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
 225 230 235 240

Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
 245 250 255
 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
 260 265 270
 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
 275 280 285
 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
 290 295 300
 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
 305 310 315 320
 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu
 325 330 335
 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr
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 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu
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 20 25 30
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 35 40 45
 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
 50 55 60
 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
 65 70 75 80
 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
 85 90 95
 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
 100 105 110
 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
 115 120 125
 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His

130		135		140
Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val				
145		150		155 160
Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu				
	165		170	175
Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr				
	180		185	190
Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met				
	195		200	205
Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly				
	210		215	220
Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn				
	225		230	235 240
Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr				
	245		250	255
Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn				
	260		265	270
Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn				
	275		280	285
Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu				
	290		295	300
Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe				
	305		310	315 320
Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu				
	325		330	335
Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr				
	340		345	350
Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu				
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Thr Ala Ala Val Ser Ser Ser Phe Arg Cys Ala Leu Ile Lys Thr Gly
 35 40 45
 Phe Gln Phe Tyr Tyr Leu Pro Ala Val Tyr Ile Leu Val Phe Ile Ile
 50 55 60
 Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met Phe Val Phe His Met
 65 70 75 80
 Lys Pro Trp Ser Gly Ile Ser Val Tyr Met Phe Asn Leu Ala Leu Ala
 85 90 95
 Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu Ile Phe Tyr Tyr Phe
 100 105 110
 Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met Cys Lys Leu Gln Arg
 115 120 125
 Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile Leu Phe Leu Thr Cys
 130 135 140
 Ile Ser Ala His Arg Tyr Ser Gly Val Val Tyr Pro Leu Lys Ser Leu
 145 150 155 160
 Gly Arg Leu Lys Lys Lys Asn Ala Ile Tyr Val Ser Val Leu Val Trp
 165 170 175
 Leu Ile Val Val Val Ala Ile Ser Pro Ile Leu Phe Tyr Ser Gly Thr
 180 185 190
 Gly Ile Arg Lys Asn Lys Thr Val Thr Cys Tyr Asp Ser Thr Ser Asp
 195 200 205
 Glu Tyr Leu Arg Ser Tyr Phe Ile Tyr Ser Met Cys Thr Thr Val Ala
 210 215 220
 Met Phe Cys Ile Pro Leu Val Leu Ile Leu Gly Cys Tyr Gly Leu Ile
 225 230 235 240
 Val Arg Ala Leu Ile Tyr Lys Asp Leu Asp Asn Ser Pro Leu Arg Arg
 245 250 255
 Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr Val Phe Ala Val Ser
 260 265 270
 Tyr Ile Pro Phe His Val Met Lys Thr Met Asn Leu Arg Ala Arg Leu
 275 280 285
 Asp Phe Gln Thr Pro Glu Met Cys Asp Phe Asn Asp Arg Val Tyr Ala
 290 295 300
 Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu Asn Ser Cys Val Asp
 305 310 315 320
 Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe Arg Arg Arg Leu Ser
 325 330 335

Arg Ala Thr Arg Lys Ala Ser Arg Arg Ser Glu Ala Asn Leu Gln Ser
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Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Ser Glu Phe Lys Gln Asn
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Gly Asp Thr Ser Leu
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Thr Ile Asp Asp Phe Arg Asn Gln Val Tyr Ser Thr Leu Tyr Ser Met
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Ile Ser Val Val Gly Phe Phe Gly Asn Gly Phe Val Leu Tyr Val Leu
 35 40 45

Ile Lys Thr Tyr His Lys Lys Ser Ala Phe Gln Val Tyr Met Ile Asn
 50 55 60

Leu Ala Val Ala Asp Leu Leu Cys Val Cys Thr Leu Pro Leu Arg Val
 65 70 75 80

Val Tyr Tyr Val His Lys Gly Ile Trp Leu Phe Gly Asp Phe Leu Cys
 85 90 95

Arg Leu Ser Thr Tyr Ala Leu Tyr Val Asn Leu Tyr Cys Ser Ile Phe
 100 105 110

Phe Met Thr Ala Met Ser Phe Phe Arg Cys Ile Ala Ile Val Phe Pro
 115 120 125

Val Gln Asn Ile Asn Leu Val Thr Gln Lys Lys Ala Arg Phe Val Cys
 130 135 140

Val Gly Ile Trp Ile Phe Val Ile Leu Thr Ser Ser Pro Phe Leu Met
 145 150 155 160

Ala Lys Pro Gln Lys Asp Glu Lys Asn Asn Thr Lys Cys Phe Glu Pro
 165 170 175

Pro Gln Asp Asn Gln Thr Lys Asn His Val Leu Val Leu His Tyr Val
 180 185 190

Ser Leu Phe Val Gly Phe Ile Ile Pro Phe Val Ile Ile Ile Val Cys
 195 200 205

Tyr Thr Met Ile Ile Leu Thr Leu Leu Lys Lys Ser Met Lys Lys Asn
 210 215 220

Leu Ser Ser His Lys Lys Ala Ile Gly Met Ile Met Val Val Thr Ala
225 230 235 240

Ala Phe Leu Val Ser Phe Met Pro Tyr His Ile Gln Arg Thr Ile His
245 250 255

Leu His Phe Leu His Asn Glu Thr Lys Pro Cys Asp Ser Val Leu Arg
260 265 270

Met Gln Lys Ser Val Val Ile Thr Leu Ser Leu Ala Ala Ser Asn Cys
275 280 285

Cys Phe Asp Pro Leu Leu Tyr Phe Phe Ser Gly Gly Asn Phe Arg Lys
290 295 300

Arg Leu Ser Thr Phe Arg Lys His Ser Leu Ser Ser Val Thr Tyr Val
305 310 315 320

Pro Arg Lys Lys Ala Ser Leu Pro Glu Lys Gly Glu Glu Ile Cys Lys
325 330 335

Val

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Tyr Gly Cys Val Phe Ser Met Val Phe Val Leu Gly Leu Ile Ala Asn
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Cys Val Ala Ile Tyr Ile Phe Thr Phe Thr Leu Lys Val Arg Asn Glu
35 40 45

Thr Thr Thr Tyr Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Val
50 55 60

Phe Thr Leu Pro Phe Arg Ile Tyr Tyr Phe Val Val Arg Asn Trp Pro
65 70 75 80

Phe Gly Asp Val Leu Cys Lys Ile Ser Val Thr Leu Phe Tyr Thr Asn
85 90 95

Met Tyr Gly Ser Ile Leu Phe Leu Thr Cys Ile Ser Val Asp Arg Phe
100 105 110

Leu Ala Ile Val His Pro Phe Arg Ser Lys Thr Leu Arg Thr Lys Arg
115 120 125

Asn Ala Arg Ile Val Cys Val Ala Val Trp Ile Thr Val Leu Ala Gly

130		135		140
Ser Thr Pro Ala Ser Phe Phe Gln Ser Thr Asn Arg Gln Asn Asn Thr				
145		150		155 160
Glu Gln Arg Thr Cys Phe Glu Asn Phe Pro Glu Ser Thr Trp Lys Thr				
	165		170	175
Tyr Leu Ser Arg Ile Val Ile Phe Ile Glu Ile Val Gly Phe Phe Ile				
	180		185	190
Pro Leu Ile Leu Asn Val Thr Cys Ser Thr Met Val Leu Arg Thr Leu				
	195		200	205
Asn Lys Pro Leu Thr Leu Ser Arg Asn Lys Leu Ser Lys Lys Lys Val				
	210		215	220
Leu Lys Met Ile Phe Val His Leu Val Ile Phe Cys Phe Cys Phe Val				
	225		230	235 240
Pro Tyr Asn Ile Thr Leu Ile Leu Tyr Ser Leu Met Arg Thr Gln Thr				
		245	250	255
Trp Ile Asn Cys Ser Val Val Thr Ala Val Arg Thr Met Tyr Pro Val				
	260		265	270
Thr Leu Cys Ile Ala Val Ser Asn Cys Cys Phe Asp Pro Ile Val Tyr				
	275		280	285
Tyr Phe Thr Ser Asp Thr Asn Ser Glu Leu Asp Lys Lys Gln Gln Val				
	290		295	300
His Gln Asn Thr				
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 <213> homo sapiens

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Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Leu Ala Leu Val Gly				
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Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr				
	50		55	60
Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys				
65	70		75	80

Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His
85 90 95

Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr
100 105 110

Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp
115 120 125

Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg
130 135 140

Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Val Ala
145 150 155 160

Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn
165 170 175

His Thr Val Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His
180 185 190

Ala Leu Val Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr
195 200 205

Val Thr Cys Tyr Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg
210 215 220

Val Glu Lys Arg Leu Lys Thr Lys Ala Val Arg Met Ile Ala Ile Val
225 230 235 240

Leu Ala Ile Phe Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser
245 250 255

Val Tyr Val Leu His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln
260 265 270

Arg Ile Leu Ala Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Ser Leu
275 280 285

Asn Gly Ala Leu Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe
290 295 300

Arg His Ala Leu Cys Asn Leu Leu Cys Gly Lys Arg Leu Lys Gly Pro
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Ser Glu Leu

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Asn Gly Leu Ser Ile Tyr Val Phe Leu
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Leu Pro Phe Arg Ala Asp Tyr Tyr Leu
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Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val

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1              5              10              15

Ile Met Leu Leu
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Ile Ala Leu Val Val Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile
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Cys Tyr Leu

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Leu Pro Tyr His Thr Leu
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Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn
1              5              10              15

Pro Leu Leu Tyr Tyr Phe Ala
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Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys Lys
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Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu
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 tctcccgga tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
 atccaagcga catcgccgtg gagggggaga gcaatgggca gccggagaac aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggct ccttcttctct ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
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 gactctagag gat 733

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 1 5 10 15
 atg gaa cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca 96
 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr
 20 25 30
 att gaa aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata 144
 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
 35 40 45
 ttt ttc tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg 192
 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
 50 55 60
 cag cct tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg 240
 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
 65 70 75 80
 gcc att tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac 288
 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
 85 90 95
 tat tat ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg 336
 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
 100 105 110
 att atg tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc 384
 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
 115 120 125
 ctg acc gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt 432
 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
 130 135 140
 cgg ctt ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg 480
 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly

145	150	155	160	
atc ata tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt				528
Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser	165	170	175	
ggc tct gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc				576
Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu	180	185	190	
tat aaa att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg				624
Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val	195	200	205	
ggc tgc ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc				672
Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile	210	215	220	
att cgg gtt ctg tta aaa gtg gag gtc cca gaa tcg ggg ctg cgg gtt				720
Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val	225	230	235	240
tct cac agg aag gca ctg acc acc atc atc atc acc ttg atc atc ttc				768
Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe	245	250	255	
ttc ttg tgt ttc ctg ccc tat cac aca ctg agg acc gtc cac ttg acg				816
Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr	260	265	270	
aca tgg aaa gtg ggt tta tgc aaa gac aga ctg cat aaa gct ttg gtt				864
Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val	275	280	285	
atc aca ctg gcc ttg gca gca gcc aat gcc tgc ttc aat cct ctg ctc				912
Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu	290	295	300	
tat tac ttt gct ggg gag aat ttt aag gac aga cta aag tct gca ctc				960
Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu	305	310	315	320
aga aaa ggc cat cca cag aag gca aag aca aag tgt gtt ttc cct gtt				1008
Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val	325	330	335	
agt gtg tgg ttg aga aag gaa aca aga gta taa				1041
Ser Val Trp Leu Arg Lys Glu Thr Arg Val	340	345		

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20 25 30

Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile
35 40 45

Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu
50 55 60

Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu
65 70 75 80

Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp
85 90 95

Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg
100 105 110

Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe
115 120 125

Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe
130 135 140

Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly
145 150 155 160

Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser
165 170 175

Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
180 185 190

Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val
195 200 205

Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile
210 215 220

Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val
 225 230 235 240

Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe
 245 250 255

Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
 260 265 270

Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val
 275 280 285

Ile Thr Leu Ala Leu Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu
 290 295 300

Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu
 305 310 315 320

Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val
 325 330 335

Ser Val Trp Leu Arg Lys Glu Thr Arg Val
 340 345

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<400> 31

Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val Leu Gly
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Asn Gly Leu Ser Ile Tyr Val Phe Leu
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<400> 32

Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr
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Leu Pro Phe Arg Ala Asp Tyr Tyr Leu
 20 25

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<400> 33

Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser Val Val
1 5 10 15

Arg Phe Leu Ala Met Val
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Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu Ile Met Ala Ser Ser
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Ile Met Leu Leu
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<400> 35

Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys
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Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu
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<211> 22
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<400> 36

Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe
1 5 10 15

Leu Pro Tyr His Thr Leu
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<400> 37

Ala Leu Val Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn
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Pro Leu Leu Tyr Tyr Phe Ala
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<211> 13

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<400> 38

Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu
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Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr Thr
1 5 10

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Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr
1 5 10

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<400> 41

Thr Val His Leu Thr Thr Trp Lys Val Gly Leu Cys Lys
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<211> 14

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<213> Homo sapiens

<400> 42

Ser Glu Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser

1 5 10

<210> 43
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<400> 43

Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu
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Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys Arg
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<210> 45
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<400> 45

Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu
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 <212> DNA
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 gcagcagtcg accccagcaa agtaatagag cagagg 36

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acc ttc agc aat aac aac agc agg aac tgc aca att gaa aac ttc aag	96
Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr Ile Glu Asn Phe Lys	
20 25 30	
aga gaa ttt ttc cca att gta tat ctg ata ata ttt ttc tgg gga gtc	144
Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val	
35 40 45	
ttg gga aat ggg ttg tcc ata tat gtt ttc ctg cag cct tat aag aag	192
Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys	
50 55 60	
tcc aca tct gtg aac gtt ttc atg cta aat ctg gcc att tca gat ctc	240
Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu	
65 70 75 80	
ctg ttc ata agc acg ctt ccc ttc agg gct gac tat tat ctt aga ggc	288
Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly	
85 90 95	
tcc aat tgg ata ttt gga gac ctg gcc tgc agg att atg tct tat tcc	336
Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser	
100 105 110	
ttg tat gtc aac atg tac agc agt att tat ttc ctg acc gtg ctg agt	384
Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser	
115 120 125	
gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt cgg ctt ctg cat gtc	432
Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu Leu His Val	
130 135 140	
acc agc atc agg agt gcc tgg atc ctc tgt ggg atc ata tgg atc ctt	480
Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu	
145 150 155 160	
atc atg gct tcc tca ata atg ctc ctg gac agt ggc tct gag cag aac	528
Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn	
165 170 175	
ggc agt gtc aca tca tgc tta gag ctg aat ctc tat aaa att gct aag	576
Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys	
180 185 190	
ctg cag acc atg aac tat att gcc ttg gtg gtg ggc tgc ctg ctg cca	624
Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro	
195 200 205	
ttt ttc aca ctc agc atc tgt tat ctg ctg atc att cgg gtt ctg tta	672
Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu	
210 215 220	
aaa gtg gag gtc cca gaa tgc ggg ctg cgg gtt tct cac agg aag gca	720

Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala	
225 230 235 240	
ctg acc acc atc atc atc acc ttg atc atc ttc ttc ttg tgt ttc ctg	768
Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu	
245 250 255	
ccc tat cac aca ctg agg acc gtc cac ttg acg aca tgg aaa gtg ggt	816
Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp Lys Val Gly	
260 265 270	
tta tgc aaa gac aga ctg cat aaa gct ttg gtt atc aca ctg gcc ttg	864
Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu	
275 280 285	
gca gca gcc aat gcc tgc ttc aat cct ctg ctc tat tac ttt gct ggg	912
Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly	
290 295 300	
gag aat ttt aag gac aga cta aag tct gca ctc aga aaa ggc cat cca	960
Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro	
305 310 315 320	
gag aag gca aag aca aag tgt gtt ttc cct gtt agt gtg tgg ttg aga	1008
Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg	
325 330 335	
aag gaa aca aga gta taa	1026
Lys Glu Thr Arg Val	
340	
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Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile Phe Phe Trp Gly Val	
35 40 45	
Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln Pro Tyr Lys Lys	
50 55 60	
Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu Ala Ile Ser Asp Leu	
65 70 75 80	

Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp Tyr Tyr Leu Arg Gly
85 90 95

Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg Ile Met Ser Tyr Ser
100 105 110

Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe Leu Thr Val Leu Ser
115 120 125

Val Val Arg Phe Leu Ala Met Val His Pro Phe Arg Leu Leu His Val
130 135 140

Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly Ile Ile Trp Ile Leu
145 150 155 160

Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn
165 170 175

Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys Ile Ala Lys
180 185 190

Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val Gly Cys Leu Leu Pro
195 200 205

Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile Ile Arg Val Leu Leu
210 215 220

Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala
225 230 235 240

Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe Phe Leu Cys Phe Leu
245 250 255

Pro Tyr His Thr Leu Arg Thr Val His Leu Thr Thr Trp Lys Val Gly
260 265 270

Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val Ile Thr Leu Ala Leu
275 280 285

Ala Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu Tyr Tyr Phe Ala Gly
290 295 300

Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu Arg Lys Gly His Pro
 305 310 315 320

Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val Ser Val Trp Leu Arg
 325 330 335

Lys Glu Thr Arg Val
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<400> 56

Phe Leu Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe
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<400> 57

Val Ser Val Trp Leu Arg Lys Glu Thr Arg Val
 5 10

<210> 58
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<400> 58

Ile Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val
 1 5 10

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Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Ser Arg Asn Cys
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Ile Ile Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val
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<211> 16

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Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln
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Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr
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Phe Leu Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe
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Val Ser Val Trp Leu Arg Lys Glu Thr Arg Val
1 5 10

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Pro Ser Ile Ser Val Ser Glu Met Glu Pro Asn Gly Thr Phe
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Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu Tyr Lys

1 5 10

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<400> 72

Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys
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<210> 73
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 5 10 15

<210> 74
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Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu Gln
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<210> 75
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Met Leu Leu Asp Ser Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys
 1 5 10 15

<210> 76
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Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu
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Glu Val Pro Glu Ser Gly Leu Arg Val Ser His Arg Lys Ala Leu Thr
1 5 10 15

<210> 78

<211> 36

<212> DNA

<213> Homo sapiens

<400> 78

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<210> 79

<211> 37

<212> DNA

<213> Homo sapiens

<400> 79

cgcgggcgc ttatactctt gtttcctttc tcaacca 37

<210> 80

<211> 99

<212> DNA

<213> artificial

<220>

<223> Peptide library random oligo.

<220>

<221> misc_feature

<222> (25)..(83)

<223> wherein "n" equals A, G, C, or T

<220>

<221> misc_feature

<222> (27)..(84)

<223> wherein "b" equals G, C, or T

<400> 80

cgaagcgtaa gggcccagcc ggccnnbnnb nnbnnbnnbn nbnnbnnbnn bnnbnnbnnb 60

nnbnnbnnbn nbnnbnnbnn bnnbccgggt ccgggcggc 99

<210> 81

<211> 95

<212> DNA

<213> artificial

<220>

<223> Peptide library random oligo.

